

Serial Number: 09/229,751A

ENTERED

CRF Processing Date: 11/27/2000

Edited by:

Verified by: (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: #12
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☒ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: 79
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as
- ☐ Inserted mandatory headings, specifically:
- ☐ Corrected an obvious error in the response, specifically:
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:
- ☐ Other:

RECEIVED

DEC 11 2000

TECH CENTER 1600/2900

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

1627

RAW SEQUENCE LISTING DATE: 11/27/2000
 PATENT APPLICATION: US/09/229,751A TIME: 17:42:32

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\11272000\I229751A.raw

Does Not Comply
 Corrected Diskette Needed

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Turnbough, Charles K
 8 (ii) TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES
 9 OF
 10 BACTERIAL CELLS
 12 (iii) NUMBER OF SEQUENCES: 80
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Glenna Hendricks
 16 (B) STREET: P.O. Box 2509
 17 (C) CITY: Fairfax
 18 (D) STATE: VA
 19 (E) COUNTRY: USA
 20 (F) ZIP: 22031
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/229,751A
 C--> 30 (B) FILING DATE: 14-Jan-1999
 31 (C) CLASSIFICATION:
 33 (viii) ATTORNEY/AGENT INFORMATION:
 34 (A) NAME: Hendricks, Glenna M
 35 (B) REGISTRATION NUMBER: 32,535
 36 (C) REFERENCE/DOCKET NUMBER: turn
 38 (ix) TELECOMMUNICATION INFORMATION:
 39 (A) TELEPHONE: (703) 425-8405
 40 (B) TELEFAX: (703) 425-8406

ERRORED SEQUENCES

64 (2) INFORMATION FOR SEQ ID NO: 2:
 66 (i) SEQUENCE CHARACTERISTICS:
 67 (A) LENGTH: 21 base pairs
 68 (B) TYPE: nucleic acid
 69 (C) STRANDEDNESS: single
 70 (D) TOPOLOGY: unknown
 72 (ii) MOLECULE TYPE: DNA (genomic)
 74 (iii) HYPOTHETICAL: NO
 76 (iv) ANTI-SENSE: NO
 80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 E--> 82 AATCATTTTT TGATTAAGCC G
 W--> 83 21
 85 (2) INFORMATION FOR SEQ ID NO: 3:

RAW SEQUENCE LISTING
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```

101      (i) SEQUENCE CHARACTERISTICS:
102          (A) LENGTH: 21 base pairs
103          (B) TYPE: nucleic acid
104          (C) STRANDEDNESS: single
105          (D) TOPOLOGY: unknown
106      (ii) MOLECULE TYPE: DNA (genomic)
107      (iii) HYPOTHETICAL: NO
108      (iv) ANTI-SENSE: NO
109      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 103 AATCATTTTT TGAGGTCTCC G
W--> 104      21
127 (2) INFORMATION FOR SEQ ID NO: 5:
128      (i) SEQUENCE CHARACTERISTICS:
129          (A) LENGTH: 21 base pairs
130          (B) TYPE: nucleic acid
131          (C) STRANDEDNESS: single
132          (D) TOPOLOGY: unknown
133      (ii) MOLECULE TYPE: DNA (genomic)
134      (iii) HYPOTHETICAL: NO
135      (iv) ANTI-SENSE: NO
136      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 145 AATCATTTTC TTCCTAAGGT G
W--> 146      21
148 (2) INFORMATION FOR SEQ ID NO: 6:
149      (i) SEQUENCE CHARACTERISTICS:
150          (A) LENGTH: 21 base pairs
151          (B) TYPE: nucleic acid
152          (C) STRANDEDNESS: single
153          (D) TOPOLOGY: unknown
154      (ii) MOLECULE TYPE: DNA (genomic)
155      (iii) HYPOTHETICAL: NO
156      (iv) ANTI-SENSE: NO
157      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 166 AATCATTTTC TGTGCCGCC G
W--> 167      21
169 (2) INFORMATION FOR SEQ ID NO: 7:
170      (i) SEQUENCE CHARACTERISTICS:
171          (A) LENGTH: 21 base pairs
172          (B) TYPE: nucleic acid
173          (C) STRANDEDNESS: single
174          (D) TOPOLOGY: unknown
175      (ii) MOLECULE TYPE: peptide
176      (iii) HYPOTHETICAL: NO
177      (iv) ANTI-SENSE: NO
178      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 187 AATCATTTTC TGCCTCGTTG G
W--> 188      21
190 (2) INFORMATION FOR SEQ ID NO: 8:
191      (i) SEQUENCE CHARACTERISTICS:
```

same
errors

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Input Set : A:\PTO.txt
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```
193      (A) LENGTH: 21 base pairs
194      (B) TYPE: nucleic acid
195      (C) STRANDEDNESS: single
196      (D) TOPOLOGY: unknown
198      (ii) MOLECULE TYPE: peptide
200      (iii) HYPOTHETICAL: NO
202      (iv) ANTI-SENSE: NO
206      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 208 AATCATTTT TGCCTCCTCG G
W--> 209      21
211 (2) INFORMATION FOR SEQ ID NO: 9:
213      (i) SEQUENCE CHARACTERISTICS:
214          (A) LENGTH: 21 base pairs
215          (B) TYPE: nucleic acid
216          (C) STRANDEDNESS: single
217          (D) TOPOLOGY: unknown
219      (ii) MOLECULE TYPE: DNA (genomic)
221      (iii) HYPOTHETICAL: NO
223      (iv) ANTI-SENSE: NO
227      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 229 AATCATTTTC TGATGCCGAA G
W--> 230      21
232 (2) INFORMATION FOR SEQ ID NO: 10:
234      (i) SEQUENCE CHARACTERISTICS:
235          (A) LENGTH: 21 base pairs
236          (B) TYPE: nucleic acid
237          (C) STRANDEDNESS: single
238          (D) TOPOLOGY: unknown
240      (ii) MOLECULE TYPE: DNA (genomic)
242      (iii) HYPOTHETICAL: NO
244      (iv) ANTI-SENSE: NO
248      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 250 AATCATTTTC TGCCTACTGG G
W--> 251      21
253 (2) INFORMATION FOR SEQ ID NO: 11:
255      (i) SEQUENCE CHARACTERISTICS:
256          (A) LENGTH: 21 base pairs
257          (B) TYPE: nucleic acid
258          (C) STRANDEDNESS: single
259          (D) TOPOLOGY: unknown
261      (ii) MOLECULE TYPE: DNA (genomic)
263      (iii) HYPOTHETICAL: NO
265      (iv) ANTI-SENSE: NO
269      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 271 AATCATTTTC TTAAGGGGAC G
W--> 272      21
274 (2) INFORMATION FOR SEQ ID NO: 12:
276      (i) SEQUENCE CHARACTERISTICS:
277          (A) LENGTH: 21 base pairs
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same

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Input Set : A:\PTO.txt
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```
278      (B) TYPE: nucleic acid
279      (C) STRANDEDNESS: single
280      (D) TOPOLOGY: unknown
282      (ii) MOLECULE TYPE: DNA (genomic)
284      (iii) HYPOTHETICAL: NO
286      (iv) ANTI-SENSE: NO
290      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
E--> 292 ATTCATTTC TTCTTTGGCG T
W--> 293      21
295      (2) INFORMATION FOR SEQ ID NO: 13:
297      (i) SEQUENCE CHARACTERISTICS:
298          (A) LENGTH: 21 base pairs
299          (B) TYPE: nucleic acid
300          (C) STRANDEDNESS: single
301          (D) TOPOLOGY: unknown
303      (ii) MOLECULE TYPE: DNA (genomic)
305      (iii) HYPOTHETICAL: NO
307      (iv) ANTI-SENSE: NO
311      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
E--> 313 AATCATTTTC TGATTAGGAA G
W--> 314      21
316      (2) INFORMATION FOR SEQ ID NO: 14:
318      (i) SEQUENCE CHARACTERISTICS:
319          (A) LENGTH: 21 base pairs
320          (B) TYPE: nucleic acid
321          (C) STRANDEDNESS: single
322          (D) TOPOLOGY: unknown
324      (ii) MOLECULE TYPE: DNA (genomic)
326      (iii) HYPOTHETICAL: NO
328      (iv) ANTI-SENSE: NO
332      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
E--> 334 AATCATTTTC TGCCGACTGC T
W--> 335      21
337      (2) INFORMATION FOR SEQ ID NO: 17:
339      (i) SEQUENCE CHARACTERISTICS:
340          (A) LENGTH: 21 base pairs
341          (B) TYPE: nucleic acid
342          (C) STRANDEDNESS: single
343          (D) TOPOLOGY: unknown
345      (ii) MOLECULE TYPE: DNA (genomic)
347      (iii) HYPOTHETICAL: NO
349      (iv) ANTI-SENSE: NO
353      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 397 ATTCATTTT TGCCGCAGAA T
W--> 398      21
399      (2) INFORMATION FOR SEQ ID NO: 46:
401      (i) SEQUENCE CHARACTERISTICS:
402          (A) LENGTH: 21 base pairs
403          (B) TYPE: nucleic acid
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Input Set : A:\PTO.txt

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994 (C) STRANDEDNESS: single
995 (D) TOPOLOGY: unknown
997 (ii) MOLECULE TYPE: DNA (genomic)
999 (iii) HYPOTHETICAL: NO
1001 (iv) ANTI-SENSE: NO
1005 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1007 ACGCATCGTT TGCCTTCTCG G
W--> 1008 21
1010 (2) INFORMATION FOR SEQ ID NO: 47:
1012 (i) SEQUENCE CHARACTERISTICS:
1013 (A) LENGTH: 21 base pairs
1014 (B) TYPE: nucleic acid
1015 (C) STRANDEDNESS: single
1016 (D) TOPOLOGY: unknown
1018 (ii) MOLECULE TYPE: DNA (genomic)
1020 (iii) HYPOTHETICAL: NO
1022 (iv) ANTI-SENSE: NO
1026 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1028 GTTACTAGTA GGGGGAATGT T
W--> 1029 21
1031 (2) INFORMATION FOR SEQ ID NO: 48:
1033 (i) SEQUENCE CHARACTERISTICS:
1034 (A) LENGTH: 21 base pairs
1035 (B) TYPE: nucleic acid
1036 (C) STRANDEDNESS: single
1037 (D) TOPOLOGY: unknown
1039 (ii) MOLECULE TYPE: DNA (genomic)
1041 (iii) HYPOTHETICAL: NO
1043 (iv) ANTI-SENSE: NO
1047 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1049 AAGCTGTGGG TGATTCTCA G
W--> 1050 21
1052 (2) INFORMATION FOR SEQ ID NO: 49:
1054 (i) SEQUENCE CHARACTERISTICS:
1055 (A) LENGTH: 21 base pairs
1056 (B) TYPE: nucleic acid
1057 (C) STRANDEDNESS: single
1058 (D) TOPOLOGY: unknown
1060 (ii) MOLECULE TYPE: DNA (genomic)
1062 (iii) HYPOTHETICAL: NO
1064 (iv) ANTI-SENSE: NO
1068 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
E--> 1070 TATTCGCCTC CTCATAGGCA T
W--> 1071 21
1220 (2) INFORMATION FOR SEQ ID NO: 57:
1222 (i) SEQUENCE CHARACTERISTICS:
1223 (A) LENGTH: 21 base pairs
1224 (B) TYPE: nucleic acid
1225 (C) STRANDEDNESS: single

same

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1226      (D) TOPOLOGY: unknown
1228      (ii) MOLECULE TYPE: DNA (genomic)
1230      (iii) HYPOTHETICAL: NO
1232      (iv) ANTI-SENSE: NO
1236      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
E--> 1238 TCGTATCCTC CGTATTTGA T
W--> 1239      21
1241 (2) INFORMATION FOR SEQ ID NO: 58:
1243      (i) SEQUENCE CHARACTERISTICS:
1244          (A) LENGTH: 21 base pairs
1245          (B) TYPE: nucleic acid
1246          (C) STRANDEDNESS: single
1247          (D) TOPOLOGY: unknown
1249      (ii) MOLECULE TYPE: DNA (genomic)
1251      (iii) HYPOTHETICAL: NO
1253      (iv) ANTI-SENSE: NO
1257      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
E--> 1259 CTTTGTGCG CTCTGCATCG T
W--> 1260      21
1262 (2) INFORMATION FOR SEQ ID NO: 59:
1264      (i) SEQUENCE CHARACTERISTICS:
1265          (A) LENGTH: 21 base pairs
1266          (B) TYPE: nucleic acid
1267          (C) STRANDEDNESS: single
1268          (D) TOPOLOGY: unknown
1270      (ii) MOLECULE TYPE: DNA (genomic)
1272      (iii) HYPOTHETICAL: NO
1274      (iv) ANTI-SENSE: NO
1278      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
E--> 1280 TTTGATTCTC CGCTTCGTCG G
W--> 1281      21
1662 (2) INFORMATION FOR SEQ ID NO: 78:
1664      (i) SEQUENCE CHARACTERISTICS:
1665          (A) LENGTH: 7 amino acids
1666          (B) TYPE: amino acid
1667          (C) STRANDEDNESS: single
1668          (D) TOPOLOGY: unknown
1670      (ii) MOLECULE TYPE: peptide
1672      (iii) HYPOTHETICAL: NO
1674      (iv) ANTI-SENSE: NO
1678      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:
1680      Phe Asp Ser Pro Leu Arg Arg
1681      1          5
1683 (2) INFORMATION FOR SEQ ID NO: 79:
1685      (i) SEQUENCE CHARACTERISTICS:
1686          (A) LENGTH: 7 amino acids
1687          (B) TYPE: amino acid
1688          (C) STRANDEDNESS: single
1689          (D) TOPOLOGY: unknown

```

same

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt

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1691 (ii) MOLECULE TYPE: peptide
1693 (iii) HYPOTHETICAL: NO
1695 (iv) ANTI-SENSE: NO
E--> 1699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79
1701 Trp Ser Pro Leu His Lys His
1702 1 5
E--> 1704 (2) INFORMATION FOR SEQ ID NO: 80:
1706 (i) SEQUENCE CHARACTERISTICS:
1707 (A) LENGTH: 12 amino acids
1708 (B) TYPE: amino acid
1709 (C) STRANDEDNESS: single
1710 (D) TOPOLOGY: unknown
1712 (ii) MOLECULE TYPE: peptide
1714 (iii) HYPOTHETICAL: NO
1716 (iv) ANTI-SENSE: NO
1720 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:
1722 Asn His Phe Leu Lys Ser Gln Pro Gly Val Val Thr
1723 1 5 10

OK

VERIFICATION SUMMARY DATE: 11/27/2000
PATENT APPLICATION: US/09/229,751A TIME: 17:42:33

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I229751A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:82 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:103 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:3
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:5
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:166 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:6
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:7
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:208 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:8
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:229 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:9
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:250 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:10
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:11
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:292 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:12
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:313 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:13
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:334 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:14
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:397 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:17
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:1007 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:46
L:1008 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:1028 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:47
L:1029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:47
L:1049 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:48
L:1050 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:1070 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:49
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:1238 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:57
L:1239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:1259 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:58
L:1260 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58
L:1280 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:59
L:1281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:59
L:1301 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:60
L:1302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60
L:1322 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:61
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:61
L:1343 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:62
L:1344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:62

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PATENT APPLICATION: US/09/229,751A DAIE: 11/27/2000
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Input Set : A:\PTO.txt
Output Set: N:\CRF3\11272000\I229751A.raw

L:1364 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:63
L:1365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:63
L:1385 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:64
L:1386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:1406 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:65
L:1407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65
L:1427 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:66
L:1428 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66
L:1449 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:67
L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67
L:1470 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:68
L:1471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:68
L:1491 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:69
L:1492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:69
L:1512 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:70
L:1513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:1533 M:254 E: No. of Bases conflict, Input:0 Counted:21 SEQ:71
L:1534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:71
L:1699 M:212 E: (34) Invalid or duplicate Sequence ID Number, Data={79:}
L:1704 M:216 E: (34) Seq. #s missing, 81 thru 79